

alignment_scores: Quality: 1929.00 Length: 356
 Ratio: 5.419 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-08-917-710-2 x AAV23659 ..

Align seg 1/1 to: AAV23659 from: 1 to: 2155

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1 MetThrLeuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuG1 17
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303 ATGACACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 352
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17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34
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353 AAGTGATGCTTCAGAACGGCTGCATGCTGGGGAGCTAGACACCATGAGGC 402
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34 InIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
|||||
403 AAATCCAGTGTGTTGAGATGACCCAGCTGCATCAAGTCCACTCTTTT 452
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51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeuTh 67
|||||
453 GAACACTTCTTGAATTCACACTACAGACAGCCCATTCACCTGCGCTTAC 502
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67 rLeuIleTrpTrpTrpThrLysGlnAspArgAspLeuGluProIleA 84
|||||
503 TCTGATCTGTGATTGACTAAGCAGCAGCGGACCTTGAGAGCCCAATTA 552
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84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
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553 ACTTCCGCCCTCCCGAGAACCGCATTTAGTAAAGGAAAGATGTCGTGG 602
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101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuAr 117
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603 TTCGGGCCACTCTCTCAATGACACGCGCACTGATACCTGCAATGTTAAG 652
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117 gAsnThrThrTyrCysSerLysValAlaPheProLeuGluValValGlnL 134
|||||
653 GAACACTACATATTGACGCAAAAGTTGCATTTCCCTTGAAAGTGTCAA 702
|||||
134 yAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTrp 150
|||||
703 AAGACAGCTGTTCAATTCCTCCCATGAACCTCCAGTGAATAACTGTAT 752
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151 IleGluTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTrpH 167
|||||
753 ATAGAAATATGGCATTCAAGAGATCACTTGTCCAATGTAGATGATATTT 802
|||||
167 eProSerSerValLysProThrIleThrTrpTyrMetGlyCysTrpLysI 184
|||||
803 TCCTTCCAGTGTCAAACCGACTATCACTTGTATATGGCTGTATATAAA 852
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184 legInAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
|||||
853 TAGAGAAATTTAATATGATATACCCGAGGTATGAACTGAGTTCTCTC 902
|||||
201 IleAlaLeuIleSerAsnAsnGlyAsnTrpThrCysValValThrTrpR 217
|||||
903 ATTGCTTAATTTCAAAATATGAAATTTACACATGTGTGTATACATATTC 952
|||||
217 oGlaAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234
|||||
953 AGAAATATGACGTACGTTTCTCATCCACAGACTCTGACTGTAAAGTAG 1002
|||||
234 aIlglySerProLysAsnAlaValProProValIleHisSerProAsnAsp 250
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1003 TAGGCTGTCCAAAATATGACAGTGCCTGTGATCATTCACCTAAATGAT 1052
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251 HisValValTrpGluLysGluProGlyGluGluLeuLeuIleProCysTh 267

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1053 CATGGGTCTATGAGAAAGAACGAGAGAGAGCTACTCATTCCTGTAC 1102
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267 rValTrpPheSerPheLeuMetAspSerArgAsnGluValTrpTrpThrI 284
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1103 GGTCTATTATTGTTTCTGATGATTTCTCGCAATGAGAGTTGGTGACCA 1152
|||||
284 leAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
|||||
1153 TTGATGGAAGAAAAACCTGATGACATCACTATTTGATGTCACCATTAACGA 1202
|||||
301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSe 317
|||||
1203 AGTATTAAGTCAATAGTAGAACAGAAAGATGAAACTGAACTCAGATTTGAG 1252
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317 rIleLysValValThrSerGluAspLeuLysArgSerTrpValCysHisA 334
|||||
1253 CATCAAGAAAGATTACTCTTGAGGATCTCAAGCGACATATGTCGTATG 1302
|||||
334 leArgSerAlaLysGlyLysValAlaLysAlaValValLysGluLys 350
|||||
1303 CTAGAAAGTGCAGAAAGCGAGTGGCAAGACAGCCAGGTGAACAGCAAAA 1352
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351 GlyAsnArgCysGlyGln 356
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1353 GGTATAGATGCGGTACG 1370
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA09048
seq_documentation_block:
ID AAA09048 standard; DNM: 2733 BP.
XX
XX AAA09048:
AC
XX
XX 01-AUG-2000 (first entry)
DE
XX Fusion polypeptide 569, IL-1 trap coding sequence.
XX
XX IL-1 trap: cytokine; antagonist; CNTF; receptor; fusion protein;
XX cytosolic; immunomodulator; osteopontin; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO200018932-A2.
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999: 99WO-US22045.
XX
XX 25-SEP-1998: 98US-0101858.
XX
XX 19-MAY-1999: 99US-0313942.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX
XX WPI: 2000-293165/25.
XX
XX P-PSDB: AAY92206.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases
XX or disorders encodes a fusion polypeptide capable of binding a cytokine
XX to form a nonfunctional complex
XX
XX Example 6: Fig 26A-E; 152pp; English.
XX
XX This sequence encodes fusion polypeptide 569, which is capable of
XX binding cytokine IL-1 to form a non-functional complex.
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the

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PR 23-JAN-1995; 95US-0376268.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Chizzone RA, Ju GW;
 XX WPI; 1996-362691/36.
 DR P-PSDB; AAM01912.
 XX Isolated interleukin-1 receptor accessory protein - used to develop
 PT prods. to treat or prevent inflammatory or immunological activities
 PT of interleukin-1
 PS Claim 9; Page 80-81, 115pp; English.
 CC A cDNA clone (AAT32027) codes for a soluble form (AAM01912) of the
 CC human interleukin-1 receptor accessory protein (IL-1R ACP), a
 CC protein that inhibits the ability of IL-1 to bind to, or otherwise
 CC activate IL-1R, esp. the Type 1 IL-1R. It was obt'd. by PCR
 CC amplification (see also AAT32029-30) of cDNA (AAT32026) coding for the
 CC extracellular domain of IL-1R ACP (AAM01911). The soluble protein
 CC was expressed in Sf9 insect cells using a baculovirus system. It
 CC can be used to treat or prevent the inflammatory or immunological
 CC activities of IL-1, and also to screen for IL-1 antagonists.
 XX
 SQ Sequence 1077 BP; 326 A; 234 C; 232 G; 285 T; 0 other;

alignment_scores:
 Quality: 1883.00 Length: 350
 Ratio: 5.395 Gaps: 0
 Percent Similarity: 99.714 Percent Identity: 99.429

alignment_block:
 us-08-917-710-2 x AAT32027 ..

Align seg 1/1 to: AAT32027 from: 1 to: 1077

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 51 AAGGATGCGCTCAGAAAGCGTGGATGACTGGGGACTAGACACCATGAGGC 100
 34 IuIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
 101 AAATCCAAAGTGTGGAAGATGAGCCACCTGCGATCAAGTCCCACTCTTT 150
 51 GluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuTh 67
 151 GAACACTTCTTGAAATTCACCTACAGCAGACCCATTACAGCTGGCCTTAC 200
 67 rIleuIleTrpTyrTrpThrLysGlnAspArgAspLeuGluGluProIleA 84
 201 TCTGATCTGGATTGACTAGCAGACCGGACCTTGAGAGGCAATTA 250
 84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 251 ACTTCGCGCTCCCGAGAACCGCATTTAGTAAAGAGAAAGATGCTCTGGG 300
 101 PheArgProThrIleuLeuAsnAspThrGlyAsnTyrThrCysMetLeuAr 117
 301 TTCGCGCCCACTCTCTCAATGACACTGGCAACTATACCTCACTGTTAAG 350
 117 .GAsnThrThrTyrCysSerLysValAlaPheProLeuGluValGlnL 134
 351 GAACACTACATATTCACAGCAAAAGTTGCAATTCCTTGGAAGTGTGTCAA 400
 134 yAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTyr 150
 401 AAGACAGCTGTTCAATTCCCATGAAACTCCAGTGCATTAACCTGAT 450

151 IleGluTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTyrPhe 167
 451 ATGACATATGCACTTCAGAGATCAGCTGTCCAAAGTAACTAGATATTT 500
 167 eProSerSerValLysProThrIleThrTyrPheMetGlyCysTyrLys 184
 501 TCTTCCAGTGTCAAAACCGACTATCAGCTGTATATGGCTGTATATAAAA 550
 184 IeGlnAsnPheAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 551 TACAGAAATTTTAAATATGATATACCCAGAGGTATGAACCTTGAGTTTCTC 600
 201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrP 217
 601 ATGCGCTTAATTTCAAAATATGAAATTAACATCATGTGTGTACATATCC 650
 217 cGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234
 651 AGAAATATGAGCTAGCTTCATCTCACAGAGACTCTGACTGTAAAGTAG 700
 234 aGlySerProLysAsnAlaValProProValIleHisSerProAsnAsp 250
 701 TAGGCTCTCCAAAAATGCACTGCCCCCTGTGATCCATTCACCTAATGAT 750
 251 HisValValTyrGluLysGluProGlyGluGluLeuLeuIleProCysTh 267
 751 CATGTGCTATGAGAAAGAACAGAGAGAGAGCTACTCATCTCCCTGTAC 800
 267 rValTyrPheSerPheLeuMetAspSerArgAsnGluValTrpTrpThr 284
 801 GGTCTATTTTATGTTTCTGATGATCTTCGCCAATGAGTTTGGTGACCA 850
 284 IeAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
 851 TTGATGGAAGAAAAACCTGATGATGATCATCTATGATGATCACTTAACGAA 900
 301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSe 317
 901 AGTATAGCATCATGTAAGAACAGATGAACAGAACTCAGATTTTGAG 950
 317 rIleLysLysValThrSerGluAspLeuLysArgSerTyrValCysHis 334
 951 CATCAAGAAAGATTACCTCTGAGAGATCTCAAGCGCATGTCTGTATG 1000
 334 IArgSerAlaLysGlyGluValAlaLysAlaAlaLysValLysGlnLys 350
 1001 CTAGCAAGTCCCAAGCGCAAGTTGCCAAAGCAGCCAGGTGACGCGA 1050
 seq_name: /SIBS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:AAT32026
 seq_documentation_block:
 ID AAT32026 standard; cDNA: 1713 BP.
 XX
 AC AAT32026;
 XX
 DT 14-OCT-1996 (first entry)
 XX
 DE Human interleukin-1 receptor accessory protein cDNA.
 XX
 KW Interleukin-1 receptor accessory protein; IL-1 antagonist;
 KW inflammation; therapy; antiinflammatory; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 Key Location/Qualifiers
 FH 1..60
 FT sig_peptide /*tag= a
 FT mat_peptide 61..1710
 FT /*tag= b
 XX
 PN WO9623067-A1.
 XX

01-AUG-1996.
 17-JAN-1996; 96MO-EP00181.
 23-JAN-1995; 95US-0376268.
 (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Chlazonite RA, Ju GW;
 WPI: 1996-362691/36.
 P-PSDB: AAM01911.

Isolated interleukin-1 receptor accessory protein - used to develop
 prods. to treat or prevent inflammatory or immunological activities
 of interleukin-1

Claim 2; Page 71-72; 115pp; English.

A cDNA clone (AAT32026) codes for human interleukin-1 receptor
 accessory protein (IL-1R AcP), a protein that inhibits the
 ability of IL-1 to bind to or otherwise activate the IL-1R.
 esp. the Type 1 IL-1R. It was obt'd. from a human YT cell cDNA
 library using a probe derived from a human partial genomic clone.
 The cDNA can be used for the prodn. of pure IL-1R AcP by expression
 in a host cell. The IL-1R AcP is used to treat or prevent the
 inflammatory or immunological activities of IL-1.

Sequence 1713 BP; 502 A; 358 C; 405 G; 448 T; 0 other;

alignment_scores:
 Quality: 1883.00 Length: 350
 Ratio: 5.395 Gaps: 0
 Percent Similarity: 99.714 Percent Identity: 99.429

alignment_block:

US-08-917-710-2 x AAT32026 ..

Alignr seg 1/1 to: AAT32026 from: 1 to: 1713

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17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34
51 AAGTATGCTCTCAGAACCGCTCGATGACTGGGACTACACACCATGAGCC 100
34 InileGluValPheGluAspGluProAlaArgIleIleCysProLeuPhe 50
101 AAATTCAGCTGTTGAGATGAGCAGCTCGATCAATCAAGTCCACTCTTT 150
51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeuTh 67
151 GAACACTCTTGAATTCACACTACAGCAGCACCACATTCAGTGCCTTAC 200
67 rLeuIleTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 84
201 TCTGATCTGATATTGACTAGCAGGAGCCGAGCTTGAGAGGCAATTA 250
84 snPheArgLeuProGluAsnArgIleSerLysGlyLysAspValLeuTrp 100
251 ACTTCGCGCTCCCGAGAACCGCATTTAGTAGAGAGAAAGATGCTGTGG 300
101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuAr 117
301 TTCGCGCCACTCTCTCAATGACACAGGCACTATACCTGACATTTAAG 350
117 gAsnThrThrTrpCysSerLysValAlaPheProLeuGluValAlaGln 134
351 GAACACTACATATTGACAGCAAAAGTTGATTCCTTGAGAGTTGTCAAA 400

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134 ysAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTrp 150
401 AAGACAGCTGTTTCATTCATCCCATGAAACCTCCAGTGCATTAACGTAT 450
151 lIleGlyTrpGlyIleGlnArgIleThrCysProAsnValAspGlyTrp 167
451 ATGAGATATGCGATTCACAGCATCTGTCCAAATGATGATGATATTT 500
167 eProSerSerValLysProThrIleThrTrpTrpMetGlyCysTrpLysI 184
501 TCCTTCCAGTGTCAAAACCGACTATCAGTGTATATGAGGCTGTATATAA 550
184 lGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
551 TACGAAATTTAATATGATATATACCCGAAAGGATGAACTGAGATTCTC 600
201 lIleAlaLeuIleSerAsnAsnGlyAsnTrpThrCysValValThrTrp 217
601 ATGCGCTTAATTTCAATTAATGAAATTTACACATGTGTGTACATATCC 650
217 cGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234
651 AGAAATGAGAGCTAGCTTTCATCTCACAGGAGCTGACTGATAAGGTAG 700
234 aGlySerProLysAsnAlaValProProValIleHisSerProAsnAsp 250
701 TAGCTCTCCAAATAATGACAGTCCCTGATCCATTCACCTAATGAT 750
251 HisValValTrpGluLysGluProGluGluGluLeuLeuIleProCysTh 267
751 CATGTGCTATGAGAAAGAACGAGAGAGAGTACTATCTCCCTGTAC 800
267 rValTrpPheSerPheLeuMetAspSerArgAsnGluValTrpTrpThr 284
801 GGCTATTATTGATTTCTGATGATTCCTCCAAATGAGATTTGGTGAGCA 850
284 lAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300
851 TTGATGAGAAAAAACCTGATGACATCTCATTTGATGTCACCATTAACGA 900
301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeu 317
901 AGATTAAGTCATAGTAGACAGAAAGATGAACAAGAACTCAGATTTGAG 950
317 rIleLysLysValThrSerGluAspLeuLysArgSerTrpValCysHisA 334
951 CATCAAGAAAGTTACCTCTGAGATCTCAAGCCGACCTATGTGTGATG 1000
334 lAspSerAlaLysGlyGluValAlaLysAlaLysValLysGlnLys 350
1001 CTGAAAGTGGCAAAAGGGAAGTTGCCAAAGCAGCCAAAGTGACGAGAA 1050

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seq_name: /SIDSt/gcgcdata/geneseq/geneseq-emb1/NA1996.DAT.AAT32028

seq_documentation_block:
 ID AAT32028 standard; cDNA: 1713 BP.
 XX AAT32028;
 AC 14-OCT-1996 (first entry)
 XX
 DE Mouse interleukin-1 receptor accessory protein cDNA.
 XX
 KW Interleukin-1 receptor accessory protein; IL-1 antagonist;
 KW inflammation; therapy; antiinflammatory; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 1..60
 FT mat_peptide 61..1710
 FT /*tag= a
 FT /*tag= b

XX W09623067-A1.
 XX 01-AUG-1996.
 XX 17-JAN-1996; 96WO-EP00181.
 XX 23-JAN-1995; 95US-0376268.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX Chlazonite RA, Ju GM;
 XX WPI: 1996-362691/36.
 XX P-PSDB; AAM01913.
 XX Isolated interleukin-1 receptor accessory protein - used to develop
 XX prods. to treat or prevent inflammatory or immunological activities
 XX of interleukin-1
 XX
 XX Example 7; Page 76-77; 115pp; English.
 XX A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor
 XX accessory protein (IL-1R ACP), a protein that inhibits the
 XX ability of IL-1 to bind to, or otherwise activate, the IL-1R,
 XX esp. the type 1 IL-1R. It was obtd. by screening cell-surface
 XX proteins in COS-7 cells transfected by 3T3-IL cDNA using
 XX anti-murine IL-1R ACP monoclonal antibody 4C5, and isolation of
 XX cDNA clones from positive lines. The murine cDNA was used to
 XX obtain a partial genomic clone of the human homologue. A probe
 XX derived from this genomic clone was then used to isolate the
 XX full-length cDNA (AAT32026) for human IL-1R ACP (AAM01911).
 XX
 XX Sequence 1713 BP; 473 A; 386 C; 428 G; 426 T; 0 other;
 XX

alignment_scores:
 Quality: 1660.00 Length: 350
 Ratio: 4.955 Gaps: 0
 Percent Similarity: 95.714 Percent Identity: 84.857

alignment_block:
 US-08-917-710-2 x AAT32028 ..

Align seg 1/1 to: AAT32028 from: 1 to: 1713

1 MethrleuLeuTrpCysValValSerLeuTrpPheTrpGlyIleLeuG1 17
 1 ATGGGACTTCTGTGTGATTTGATGAGTCTGTCTTATGAGATCCGCA 50
 17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34
 51 GAGTCATGCTTCGAGCGCTGTGATGACTGGGAGCTAGATACCATGGAC 100
 34 InileglnValPheGluAspLeuProAlaArgIleLysCysProLeuPhe 50
 101 AATCCAAAGTGTGGAAGATGAGCGGCTGCAATCAAGTGCCTCTTT 150
 51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerIleGlyLeuTh 67
 151 GAACACTTCTCGAAGTACACTACGACATGCCATTCCTCTGCTGCTTAC 200
 67 rLeuIleTrpTrpThrLysGlnAspArgAspLeuGluLeuIleA 84
 201 CCGATCTGCTAGTACGACCAAGACCGGAGCTGAGAGCCCATTA 250
 84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
 251 ACTTCGCCCTCCAGAGATCGCATCACTAAGAGAAAGATGCTCTGG 300
 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeuAr 117
 301 TTCGGGCCCTCTCTCAATGACAGGGCAATTACACCTGCTGATTGAG 350

117 gAsnThrThrTrpCysSerLysValAlaPheProLeuGluValValGlnL 134
 351 GACACAACTTACTGTCGACCAAGAGTTCATTTCCCTGGAAGTGTGTAGA 400
 134 ysAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTrp 150
 401 AGGACAGCTGTTTCAATTTGCTGCATGAGATTCCAGTGCACAAAGATGTAT 450
 151 lIeGluTrpGlylIeGlnArgIleThrCysProAsnValAspGlyTrpPh 167
 451 ATTGAACTGGCATTCATATGATCAGATCCAAATGTATGACGATCTT 500
 167 eProSerSerValLysProThrIleThrTrpTrpMetGlyCysTrpLysI 184
 501 TCCTTCGAGTGTCAACCATGCGTACTGTGTATAAGGTTGACTGAAA 550
 184 lIeGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 200
 551 TAGTGACTTTCATATGATGATGACTACCGAGGCGATGAACTGACTTTTC 600
 201 lIeAlaLeuIleSerAsnAsnGlyAsnTrpThrCysValValThrTrpPr 217
 601 ATCCCTTGTTGTTCAATTAACGGAATTAACATGTGTGTATATATCC 650
 217 oGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 234
 651 TGAAAGGAGAGCTCTTCACTCACCACGAGAGCTGCTGCTAAAGGTGG 700
 234 aGlySerProLysAsnAlaValProProValIleHisSerProAsnAsp 250
 701 TGGGCTCACAAAGATGATGCTCCACCCAGACTTATCTCCAAATGAC 750
 251 HisValValIleTrpGluLysGluProGlyGluGluLeuLeuIleProCysTh 267
 751 CGTGTGTCTATGAGAAAGAACACGAGAGAGAGACTGTATTCCTGTGAA 800
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 901 AGTGTAGTATTATTTCACAGGAGATGAAACAGGACTCAGATTGTGAG 950
 317 rIleLysLysValThrSerGluAspLeuLysArgSerTrpValCysHisA 334
 951 CATCAAGAAAGTCAACCCGAGAGATCTCAGGCAACATGTCTGTCTATG 1000
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 1001 CTCGAAATATCCAAAGGGAAGCTGAGCAGGCTGCCAAGGTGAACAGAAA 1050

seq_name: /SIDS1/gcdata/geneseq/geneseq-emb1/NA2001A.DAT:AA124540

seq_documentation_block:
 ID AA124540 standard; DNA; 287 BP.
 XX AA124540;
 AC
 DX 12-OCT-2001 (first entry)
 DE
 XX
 DE Probe #14473 for gene expression analysis in human cervical cell sample.
 KW Probe: human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 OS
 XX Homo sapiens.
 XX

PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00670.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 25; SEQ ID No 14473; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging
 CC of diseases of the cervix, notably cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other.
 XX
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 Ratio: 5.558 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.947
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 53 AGATGAGCCAGCTGCGATCAGTGCCTTTGAAACACTTCTTGAAAT 102
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 56 heAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrT 72
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 103 TCAACTACAGCACAGCCCATTCAGCTGCTTACTGATCGATGCTATTTGG 152
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 73 ThrLysGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProG1 89
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 153 ACTAGGCGAGACCGGACCTTGAGAGCCCAATTAACCTCCGCCCTCCCGA 202
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 89 uAsnArgIleSerLysGluLysAspValLeuTyrPheArgProThrLeu 106
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 203 GAACCGCATTAAGTAAGGAAAGATGCTGTGTTCCGCCCTCCCTCC 252
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 106 euAsnAspThrGlyAsnTyrThrCysMetLeuArg 117
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 253 TCAATGACACTGGCACTATACATGCTTAAGG 287

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAI49786
 seq_documentation_block:
 ID AAI49786 standard; DNA: 287 BP.
 XX
 AC AAI49786;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Probe #18472 used to measure gene expression in human placenta sample.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 XX genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-48897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 XX
 PS Claim 25; SEQ ID No 18472; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders.
 XX
 SQ Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other.
 XX
 alignment_scores:
 Quality: 528.00 Length: 95
 Ratio: 5.558 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.947
 XX
 alignment_block:
 US-08-917-710-2 x AAI49786 ..
 XX
 Align seg 1/1 to: AAI49786 from: 1 to: 287
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 23 ArgCysAspAspPTrpGlyLeuAspThrMetArgGlnIleGlnValPheG1 39
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 3 CGCTGCGATGACTGGGACTAGACACCATGAGCAAAATCCAAAGTGTGA 52
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 39 uAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysP 56
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 53 AGATGAGCCAGCTGCGATCAGTGCCTTTGAAACACTTCTTGAAAT 102
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 56 heAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIleTyrTyrT 72
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 103 TCAACTACAGCACAGCCCATTCAGCTGCTTACTGATGCTATTTGG 152
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 73 ThrLysGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProG1 89


```

|||||
153 ACTAGGACGAGACCGGAGCCTTGAGAGCAATTAACCTCCGCCGCCA 202
89 uasnaqgllieserlysglulysaspvalleutrphearprothleul. 106
|||||
203 GAACCGCATTTAGTAAGAGAGATGTGCTGCGTCCGCCACACTCTCC 252
106 euasnaqphrthglyasntrythrlycsmelleuarg 117
|||||
253 TCATATGACACTGGCACTATACCTGATGTAAAG 287
seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAx58245

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seq_documentation_block:

ID AAx58245 standard; CDNA: 2061 BP.

AAx58245;

22-JUL-1999 (first entry)

Human IL-1RD8 coding sequence.

IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNAX; therapy;

IL-1 receptor-like protein; abnormal expression; immunological disorder;

inflammatory disorder; morphological disorder; ss.

Homo sapiens.

WO919480-A2.

22-APR-1999.

14-OCT-1998; 98WO-US20939.

10-AUG-1998; 98US-0095987.

15-OCT-1997; 97US-0951829.

17-NOV-1997; 97US-0971635.

12-MAR-1998; 98US-0078008.

18-MAR-1998; 98US-0040714.

15-APR-1998; 98US-0081883.

(SCHE) SCHERING CORP.

Bazan JF, Debets JEMA, Kastelein RA, Sana TR, Timans JC;

WPI: 1999-326545/27.

P-PSDB; AAY14128.

Interleukin-1 receptor-like polypeptides RDB, 9 and 10

Claim 28; Page 93-96; 150pp; English.

This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide,

designated IL-1 receptor DNAX designation 8 (IL-1RD8), of the

invention. The IL-1RD8, IL-1RD9, and IL-1RD10 proteins, their fragments

and mutants, also related antibodies, other binding agents and

(ant)agonists are used to treat conditions associated with abnormal

expression of the polypeptide or abnormal expression of, or response to,

their ligands, e.g. immunological, inflammatory or morphological

disorders. They may also be used to screen for binding agents (potential

drugs), diagnostic reagents (to detect the proteins or their ligands) and

to isolate related sequences. Antibodies may also be used to raise

anti-idiotypic antibodies, as carriers for toxins, radionuclides or other

therapeutic agents, and for affinity purification.

Sequence 2061 BP; 656 A; 421 C; 459 G; 525 T; 0 other;

alignment_scores:

Quality: 438.50

Ratio: 1.975

Percent Similarity: 60.163

Percent Identity: 31.978

Length: 369

Gaps: 15

Percent Identity: 31.978

alignment_block:
US-08-917-710-2 x AAx58245 ..

Align seg 1/1 to: AAx58245 from: 1 to: 2061

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1 MetThrleuLeuTrpCys...ValValSerLeuTrpPheTrpGlyLele 16
|||||
19 TTGGCCCTTGTCGTCTGTCGTGTCAGCACAATCTGAAGATGTC 68
16 uGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMet 33
|||||
69 AAAGGAATATCTGTGATGCTCATTGACTGGTCATGGAT...CTCA 115
33 rGlnIleGlnValPheGlnAspGluProAlaArgIleLeuCysProLeu 49
|||||
116 AGACATACATGCTTGGCAGCTGACAGCAGTCGAGGAATATGCCCTT 165
50 PheGluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyle 66
|||||
166 TTCTACAGTTATATTCGTACCACTATAGCACGCCGACAGACACTGGGCT 215
66 uThrLeuLeuTrpTrpTrpThrLysGlnAspArgAspLeuGluProI 83
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216 CAGCTTATGTGTATC.....AAACAAAGTGATTTGGAAGACCCA 259
83 leAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValleu 99
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260 TCATCTTT.....TCAGAGTCAGAGATGACCAAGAGAAATTCATATA 303
100 TrpPheArgProThrLeuLeuAsnAspThrGlyLysnTrpCysMetle 116
|||||
304 TGGTTCACTGACGCTGAGGACACACAGCTGATTCACCTGTGTTT 353
116 uArgAsnThrThrTrpCysSerLysValAlaPheProLeuGluValAlG 133
|||||
354 AAGCAATCAATATTCATGCAAGAGTCAATGCTGACTGTGAG 403
133 lLysAspSer.....CysPheAsnSerPrometLysLeuProValHis 147
|||||
404 AGAATGAATCAGCGCTGTGCTACCAACAGCAGATCCG..... 441
148 LysLeuTrpIleGluTrpGly.....IleGlnArgIleThrCys 160
|||||
442 .....TATTAGAAATAATCTGAATCACTAAAGAAAGAGATCCCTG 485
160 sProAsnValAspGlyTrpPheProSerSerValLysProThrIleTrp 177
|||||
486 TCCAGACATGATGACTTAAAGAGTCCGATCAGAGCCTGATGTGTGT 535
177 rPtyrMetGlyCysTrpLysIleGlnAsnPheAsnAspValIleProGlu 193
|||||
536 GGTATTAAGAAATGCAAGCCAAAATGTGAGAGCAATATATATACAGAA 585
194 GlyMetAsnLysSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTy 210
|||||
586 GGAATAGCTCTTCTGATCCAGAGATTCAGAAAGAAAGATGAGAAATTA 635
210 rThrCysValValThrTrpProGluAsnGlyArgThrPheHisLeuTrp 227
|||||
636 CACATGTGAACCTTAATAT.....GAAGAAACCTT.....GTAAAG 673
227 rGthrLeuThrValLysValIleGlySerProLysAsnAlaValPro... 242
|||||
674 GAACAACTGAATTAAGAGTTACAGCTTCTACAGACAGCAAGCTCCCAAG 723
243 ProValIleHisSerProAsnAspHisValValTyGluLysGluProG 259
|||||
724 CCAATGTTCCCATGAGATCAGCAAGTCAAGTATATGATGTCACACTGGG 773
259 yGluGluLeuLeuLeuProCysThrValTrpPheSerPheLeuMetAsp 276
|||||
774 TAAGCCTTGAAACATCCCTCGCAAGCAATTCCTTGATTCAGTGAAGAGT 823

```


CC disorders. They may also be used to screen for binding agents (potential drugs) diagnostic reagents (to detect the presence of a disease).

209 nlyrThrCysValValThrTyRProGluAsnGlyArgThrPheHisLeuT 22

618 TTACACATGTGAAGCTTAATAT.....GAAGAAACTT.....GTAA 655

```

226 hrArgThrLeuThrValIleValValGlySerProLysAsnAlaValPro 242
      ||||| .....
656 GAGCAACACATGAAATGAAAGTTACCTTACACAGCAAGCCCTCC 705
      ||||| .....
243 ...ProValIleHisSerProAsnAspHisValValTyrGluGluP 258
      ||||| .....
706 AAGCCATGTTCCCATGAGAAACACCAAGTGTATGATGTCGACGT 755
      ||||| .....
258 oGluGluLeuLeuLeuProCysThrValTyrPheSerPheLeuMet 275
      ||||| .....
756 GGGTAACCTCTGACATCCCTCAAGACATTTTCGATTCAGTGCAG 805
      ||||| .....
275 sPSeArGAsnGluValTyrTrpThrIleAspGlyLysLysProAsp 291
      ||||| .....
806 AGTCTGGCCCAATGATCTACTG...ATGAAGAGAGAAAG... 843
      ||||| .....
292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThr 308
      ||||| .....
844 .....TTATTGAGAACTGGCAGCTCACATTAGA...GA 875
      ||||| .....
308 uAspGluThrArg.....Thrg 314
      ||||| .....
876 AGGGAATAATAGCTTCTCAAGACATCTTGAGAAAAGAAAGTTGAAT 925
      ||||| .....
314 InIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSerTyr 330
      ||||| .....
926 TGGCACCATCTTGTGACTGAGTGTGAGAGCTGACTG...GCCAATTAT 972
      ||||| .....
331 ValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLysVal 347
      ||||| .....
973 ACCTGCCATGTTGAAACCGAATGAGAGGAAACATGCCAGTGTTCCT 1022
      ||||| .....
1023 GCGTAAAAAG 1032

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seq.name: /STDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAx84308

seq_documentation_block:

ID AAX84308 standard; DNA: 1979 BP.

AC AAX84308;

DT 08-SEP-1999 (first entry)

XX Human TIGIR coding sequence.

DE TIGIR: human; chromosome X; FG syndrome; premature ovarian failure-1;

KW leiomyomatosis; epilepsy; Bazex syndrome; detection; defective gene;

KW cell-signal transduction; gene therapy; inhibitor; immune regulation;

KW cell proliferation; inflammation; ss.

OS Homo sapiens.

PN W09932629-A1.

PD 01-JUL-1999.

PF 23-DEC-1998; 98WO-US27625.

PR 23-DEC-1997; 97US-0068634.

XX (IMMV) IMMUNEX CORP.

PI Sims JE;

DR WPI, 1999-418928/35.

DR P-PSDB; AAY22164.

XX New interleukin-1 receptor analog TIGIR nucleic acid and proteins

PT used to, e.g. treat autoimmune disease

XX Claim 1; Page 8-9; 79pp; English.

```

XX This sequence encodes the human TIGIR protein of the invention. The
CC TIGIR DNA sequences can be used: (a) as probes or primers for
CC identifying nucleic acid that encodes proteins with TIGIR activity;
CC (b) to identify human chromosome X, to map genes on this chromosome
CC and to identify disease-related genes (particularly in the region
CC Xq21.3-22 where genes are present associated with e.g. FG syndrome,
CC premature ovarian failure-1, leiomyomatosis, epilepsy, Bazex syndrome
CC etc.) including detection of defective genes; (c) to study cell-signal
CC transduction and the TIGIR system, and (d) in gene therapy. Sense and
CC antisense oligonucleotides derived from the TIGIR coding sequence can be
CC used to inhibit expression of the TIGIR gene. The TIGIR protein, or its
CC soluble fragments, are used: (1) to study cellular processes (immune
CC regulation, proliferation, death, migration, interaction with other cells
CC and inflammation); (1i) to identify and purify proteins that associate
CC with TIGIR ligands and receptors, and to measure their biological
CC activity; (1ii) in screening for, and rational design of, potential
CC inhibitors of activity; (1v) therapeutically against diseases mediated by
CC TIGIR polypeptide counter-structures; (v) as molecular weight markers in
CC electrophoresis; (vi) for determining isoelectric points of unknown
CC proteins; (vii) as controls for determining the extent of protein
CC fragmentation (e.g. to aid characterisation of protein structures by mass
CC spectrometry); (viii) for generation of antibodies (Ab); and (ix) to
CC deliver diagnostic or therapeutic agents to cells that express TIGIR
CC binding molecules. Ab are used for affinity purification of TIGIR;
CC therapeutically to inhibit binding of TIGIR to its counter structures,
CC and (if agonistic) to promote cell signalling.
XX
SQ Sequence 1979 BP; 636 A; 405 C; 439 G; 499 T; 0 other;

```

alignment_scores: Quality: 431.00 Length: 345
Ratio: 2.072 Gaps: 14
Percent Similarity: 60.290 Percent Identity: 32.754

alignment_block:

US-08-917-710-2 x AAX84308 ..

Align seg 1/1 to: AAX84308 from: 1 to: 1979

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24 CysAspAspTrpGlyLeuAspThrMetArgGlnIleGluValPheGluAs 40
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9 TGCATTGACTGTGCTAGTGCAT...CTCAAGACATACATAGCTTGGCAGG 55
      ||||| .....
40 pGluProAlaArgIleLysCysProLeuPheGlnHisPheLeuLysPhe 57
      ||||| .....
56 TGACACGACCGCGAGTGAATGTCCCTTTTACAGTATATTCGTACCA 105
      ||||| .....
57 sNtYserThrAlaHisSerAlaGlyLeuThrLeuIleTyrTrpThr 73
      ||||| .....
106 ACTATAGCACGCGCCGACGACTGGCTCAGCTTATGTGTAC..... 149
      ||||| .....
74 LysGluAspArgAspLeuGluIupProIleAsnPheArgLeuProGluAs 90
      ||||| .....
150 AAAACCAAGGTGATTTGGAAAGCCCATCATCTT.....TCGAGAGT 193
      ||||| .....
90 nArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeu 107
      ||||| .....
194 CAGGATGACCAAGAGAGATTCATATGTTTCACAGCTGAGGCAC 243
      ||||| .....
107 sNAspThrGlyAsnTyrThrCysMetLeuArgAsnThrTyrCysSer 123
      ||||| .....
244 AAGACAGTGAATTCATCTGTGTTTAAAGAACTCAACATATGTCATG 293
      ||||| .....
124 LysValAlaPheProLeuGluValAlaGlnLysAspSer.....CysPh 138
      ||||| .....
294 AAGGTTCATATGCTTGTGAGAGAAATGATGAGCCCTGTGCTA 343
      ||||| .....
138 eAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
      ||||| .....
344 CAACAGCAGAGATCCG.....TATTAGAAATAATCTG 375

```


CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibitor-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.

XX
 S0 Sequence 3120 BP; 913 A; 632 C; 680 G; 895 T; 0 other:

alignment_scores:
 Quality: 409.50 Length: 351
 Ratio: 1.905 Gaps: 12
 Percent Similarity: 61.254 Percent Identity: 30.484

alignment_block:
 US-08-917-710-2 x ABA09029 ..

Align seg 1/1 to: ABA09029 from: 1 to: 3120

1 MethrleuLeuTrpCysValValSerLeuTrpPheTrpGlyLeuGlu 17
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 17 nSerAspAlaSerGluArgCysAspArgPyrGlyLeuAspThrMetArg 34
 582 AAGAGGCTCCGCCGATGATGACACTGCTGTCATCATGAT...ATCAGA 628
 34 InileglnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
 629 AATATCAAGTTTGTGGAGAGCCCTGTCGAATCAATGTCACCTCTTT 678
 51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGlyLeu 67
 679 TATGCTTATATCAGACAAATTTACTCCCTTGCCCAAGTGTGTCAG 728
 67 rLeuIleTrpTrpThrLysGlnAspArgAspLeuGluProIleA 84
 729 TTTGATGCTGACAAAGTTCTGCTCGAGACTTTGAGAGAGCCATAG 778
 84 snPheArgLeuProGluAsnArgIleSerLysGlnLysAspValLeuTrp 100
 779 CCTTT.....GACGGAAGTAGAATGAGCAAGAAAGAAAGACTCCATTGG 822
 101 PheArgProThrLeuLeuAsnAspThrGlyAsnTrpThrCysMetLeu 117
 823 TTCGGCCCAATGCTATGACAGACAGGCTCTACCGCTGTGCACAG 872
 117 gasnThrThrTrpCysSerLysValAlaPheProLeuGluValValGln 134
 873 AAAGTCCACTTACTGATGAAAGATCATCTCATGACAGAGTGGTGAAA 922
 134 ysAspSer.....CysPheAsnSerProMetLysLeuProValHisLys 148

923 ATGACACTGACTCTGCTATATTCGAAGATGAG..... 957
 149 LeuTrpIleGluTrpGly.....IleGlnArgIleThrCysPr 161
 958 ...TATTTTGAAGAAAGCTGAACTTAGCAAAACGAAAGAAATTTGATGCC 1004
 161 GAsnValAspGlyTrpPheProSerSerValLysProThrIleThrTrp 178
 1005 TGACGTAGAGGATTTTCTACGCCACAGAGAACTGAAATCTTGTGT 1054
 178 rYrMetGlyCysTrpLysIleGlnAsnPheAsnValIleProGluGly 194
 1055 ACAAGAAATGACAGACAAACAAATGAGGCCAATATGTTTCAGAAA 1104
 195 MetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnValTrpThr 211
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 211 rCysValValThrTrpProGluAsnGlyArgTrpPheHisLeuThrArg 228
 1155 CTGTGAATTAATAAT.....GGAGGCTTGTGTGAGAGAACTACTGT 1198
 228 hLeuThrValLysValValGlySerProLysAsnAlaValProProVal 244
 1199 AATTAACGTGTACA.....GCCCTGTGACTGATTAACCCCAAG 1239
 245 IleHisSerProAsnAspHis.....ValValTrpGluLysGluProG 259
 1240 CTTTGTATCTTATGAGAAAGTCAAGACATGACAGAGACCCAGCTGG 1289
 259 yGluGluLeuLeuIleProCysTrpValTrpPheSerPheLeuMetAsp 276
 1290 TGACTCTGCTATCTTAACCTGACAGACTTCTTGTGGTACAGCGAGATG 1339
 276 eArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIle 292
 1340 TCAGTCCTTAAATTTACTGATGAAAGAGAAATTTATTTGAAGATCTG 1369
 293 ThrIleAspValThrIleAsnGluSerIleSerHisSer.ArgThr.... 307
 1390 GATGAATAATCGAGTTTGGGAAGTGCATTAATTTCTTAAGAGCATC 1439
 308GluAspGluThrArgTrpGlnIleLeuSerIleLysLysValThr 322
 1440 TTGGGGAACAGAGATTTCCATCTCATTAAT...GTGAGCTGTGTGAA 1486
 323 SerGluAspLeuLysArgSerTrpValCysHisAlaArgSerAlaLysG 339
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 1534 A 1534
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 seq_documentation_block:
 ID AAK52925 standard; cDNA: 3120 BP.
 AC AAK52925;
 DT 06-NOV-2001 (first entry)
 DE Human polynucleotide SEQ ID NO 2454.
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 OS Homo sapiens.

67 rleuiletrpyrtrpThrLysGlnAspArgAspLeuGluGluProIleA 84
TTTTT||||| : : : : : |||:|||||
729 TTTATGTGGTACAAAGTTCTGGTCTTGGACACTTTGAGAGCCAAATAG 778
84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuIle 100
||| : : : : : |||:|||||
779 CCTTT.....GACGGAGATGACATAGCACAAGAGAACTCCATTGG 822
101 PheArgProThrIleuLeuAsnAspThrGlyAsnTyrThrCysMetLeuAr 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
823 TTCCGGCCAACTGGCTGACAGGACATGGTCTTACGGCTGGTCATCAG 872
117 GAsnThrThrTyrCysSerLysValAlaPheProLeuGluValGlnL 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
873 AAATCCACTTACTGTATGAAAGTATCCATCTCACTGACATGGGTGAA 922
134 yAspSer.....CysPheAsnSerProMetLysLeuProValHisLys 148
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
923 ATGACATCGACTCTCTTAATTCCAAGATGAA..... 957
149 LeuTyrIleGluTyrLys.....IleGlnArgIleThrCysPr 161
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958 ...TATTTGAAAAGCTGACTGACAAAGCAAGAAATTTATGCGC 1004
161 AsnValAspGlyTyrPheProSerSerValLysProThrIleThrPr 178
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1005 TGACATAGAGGATTTTCTACTCCACACAGAAACCTGAATCCTTTGGT 1054
178 yTretGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGly 194
||| ||| : : : : : |||:|||||:|||||:|||||:|||||
1055 ACAAGAGATGCGAGCAAAAACATGGAGCCAGATGTGATTCAAAAGA 1104
195 MetAsnLeuSerPheLeuIleAlaLeuIleSerAsnGlyAsnTyrTh 211
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1105 GATACCTCTGCTTATAAGAAAGTACAGACATGACATTGGAATTTATC 1154
211 rCysValValIThrTyrProGluAsnGlyArgThrPheHisLeuThrArg 228
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1155 CTGTGATTTAAATAT.....GGAGGCTTTGTTGTGAGAAAGACTCTG 1198
228 hrLeuThrValLysValValGlySerProLysAsnAlaValProProVal 244
||||| ||| : : : : : |||:|||||:|||||:|||||:|||||
1199 AATTAACTGTACA.....GCCCTCGACTGATTAAGCCACCCCAAG 1239
245 IleHisSerProAsnAspHis.....ValValTyrGluLysGluPro 259
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1240 CTTTGTATCTATGAGAAAGTAAATGACATTCAGAGAACCCAGCTGG 1289
259 yGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 276
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1290 TACCTCTGCTAATCTAACCTCAGAGGTTTCTTTGGTGACAGCGAGATG 1339
276 eArgAsnGluValTyrPrThrIleAspGlyLysLysProAspIle 292
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293 ThrIleAspValThrIleAsnGluSerIleSerHisSerArgThr.... 307
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1534 A 1534

seq_documentation_block:

ID AAI15283 standard; DNA; 478 BP.

AC AAI15283;

DT 12-OCT-2001 (first entry)

DE Probe #5216 for gene expression analysis in human cervical cell sample.

KW Probe: human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer; ss.

OS Homo sapiens.

PN WO200157278-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488901/53.

PT Human genome-derived single exon nucleic acid probes useful for

PS analyzing gene expression in human cervical epithelial cells -

PS Claim 25; SEQ ID No 5216; 487bp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SEN). The present sequence is one such probe. The SENs are derived

CC from human HeLa cells. The SENs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging

CC of diseases of the cervix, notably cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;

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Quality: 398.00

Ratio: 5.528

Percent Similarity: 100.000

Percent Identity: 98.611

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seq_documentation_block:
Sequence 1, Application US/09173151A
Patent No. 6326472
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200

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seq_documentation_block:
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: Patent No. 6326472
GENERAL INFORMATION:
: APPLICANT: Timans, Jacqueline C.
: APPLICANT: Debets, Johannes Eduard Maria
: APPLICANT: Antonius
: APPLICANT: Sana, Theodore R.
: APPLICANT: Bazan, J. Fernando
: APPLICANT: Kastelein, Robert A.
: TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNA Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
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: FILING DATE: 15-APR-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/095,987
: FILING DATE: 10-AUG-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/078,416
: FILING DATE: 18-MAR-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/062,066
: FILING DATE: 15-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0767X
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650)852-9196
: TELEFAX: (650)496-1200
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2537 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..2004
: US-09-173-151A-34

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alignment_scores:
: Quality: 411.50      Length: 330
: Ratio: 2.068        Gaps: 12
: Percent Similarity: 60.303      Percent Identity: 31.818

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alignment_block:
US-08-917-710-2 x US-09-173-151A-34

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7 TGCACCTGACTGTCATTCGAT...ATCAGAAATATCAAGTTTGGTGGG 53
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40 pGluProAlaArgIleLeuGlyCysProLeuPheGluHisPheLeuLysPhe 57
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54 AGACCTGCTTGCATCAATGATGTCACCTTTTATGTTATATACAGAACAA 103
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104 ATTACTCCCTGCGCCCAAGAGTGGAGCTGAGTGTGATGTTGATCAAGAA 153
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74 LysGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProGluAs 90
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154 TCTGTCTCTGGAGACTTTGAAAGCCCAATAGCCTTT...GACGGAG 197
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90 nArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeu 107
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198 TAGAATGACCAAGAAAGAGACCTCATTTGTTCCGCGCAACATTTGCTAC 247
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107 snArgThrGlyAsnTrpThrCysMetLeuArgAsnThrTrpTrpCysSer 123
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138 eAsnSerProMetLysLeuProValHisLysLeuTrpIleGluTrpGly 154
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430 CTGCCACACGAGAACCTGAAATCCTTTGTGATACAGAACTCAGAGCAAA 479
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184 eGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 201
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480 AACATGAGGCCCAAGTATTTGTTCAAAAGAGATCTGCTTTATAGAG 529
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201 IleAlaLeuIleSerAsnAsnGlyAsnTrpThrCysValValThrTrpPro 217
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530 AAGTCAGAGAAAGATGACATTTGAATTTATCTGATTAATAATAT... 576
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218 GluAsnGlyArgThrPheHisLeuThrArgThrIleThrValLysValVa 234
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577 ...GGAGGCTTTGTTGTGAGAAAGAACTGATTAATCTGTAC... 618
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619 ...GCCCTTGACTGATTAACCCACCAAGCTTTTGTATCTATGAGAA 664
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251 Is.....ValValTrpGluLysGluProGlyGluLeuLeuLeuPro 265
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282 pThrIleAspGlyLysLysProAspAspIle.....T 293
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seq_documentation_block:

Sequence 12, Application US/08091519
Patent No. 5350683
GENERAL INFORMATION:
APPLICANT: Sims, John E.
APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/091,519
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/701,415
FILING DATE:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 06-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31680
REFERENCE/DOCKET NUMBER: 2003-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Mouse
CELL LINE: 702/3
IMMEDIATE SOURCE:
LIBRARY: 702/3
CLONE: 12
FEATURE:

NAME/KEY: CDS
LOCATION: 85..1317
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 124..1314
OTHER INFORMATION:
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 85..123
OTHER INFORMATION:
US-08-091-519-12

alignment_scores:
Quality: 307.00 Length: 345
Ratio: 1.574 Gaps: 14
Percent Similarity: 56.522 Percent Identity: 26.377

alignment_block:

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38 eGluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuL 55
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55 yspHeaAspTrpSerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTy 71
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292 ..TCGACATCTCCACACAGTTCCCATAGTTTCTGACG..... 327
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184 eGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu 201
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201 leAla.....LeuIleSerAsnAsn..... 207
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208 ...GlyAsnTrpThrCysValValThrTyProGluAsnGlyArgThrPh 223

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367 .GAGCCAGAGATGGGTGAGAGGTAACTACTCTGATTCGACGAGC 415
105 euleuasnspthrglyasnlyrthrcysmelleuargasnthrlyr 121
416 TCGACGAACACTCTGTACTACTATTTGACATTAAGAAACCATCCGAC 465
122 CysSerlyValAlaPheProleuGluValGlnIlyAspSerCysph 138
466 TGTGAGCAAAATGCTGTGAGATCAAGGCTTTAG..... 501
138 easnserProMetLysLeuProValHisLysLeuTyrlleGlyrGlyr 155
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155 leGlnargIlethr.....CysProasnValAspGlyrlyrhe 167
548 CTCCTCCACACCGCGGTACTAGTGTCCCTGACCTGAAAGAAATTCATC 597
168 ProSerSerValLysProThrIleThrIlePyrMetGlyCysTyrlly 184
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184 eGlnasnheasnValIleProGlyGlyMetAsnLeuSerPheLeu 201
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201 leAla.....LeuIleSerAsnAsn..... 207
674 GTGACGAGAGACCCACAGCCTATTGATATCAACACGCTCATGAGAGAT 723
208 ..GlyAsnTyrlthrcysValValIleThrTyrlProGluAsnGlyrGlyr 223
724 GCAGGCTATTACAGATGTGTATGACATTTACTTAACATGACGAGATA 773
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774 CAACATCCCTGGAATATGAACTCCGGGTAAAGGACCAACCGAGAC 823
240 laValProProValIleHisSerProAsnAspHisValValTyrlGly 256
824 CCATC...CCTGTATCATTTCTCCCTGGACACATA.....CCAGCA 864
257 GluProGlyGluGluLeuLeuIleProCysThrValIlyrPheSerPhe 273
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1015 TCAGAGAAATGATGAACACTATGTGGAAGTCCGCTGATTTTATCCAGT 1064
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seq_name: /cgn2_6/ptodata/1/ina/PC/US_COMB.seq: PCT-US91-03478-12

seq_documentation_block:
; Sequence 12, Application PC/US9103478
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.

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APPLICANT: Cosman, David J.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mosley, Bruce A.
APPLICANT: Dower, Steven K.
TITLE OF INVENTION: Type II Interleukin-1 Receptors
NUMBER OF SPOUNCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03478
FILING DATE: 19910517
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/534,193
FILING DATE: 06-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,576
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,071
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31680
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-5570
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: N
ANT-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Mouse
CELL LINE: 702/3
IMMEDIATE SOURCE:
LIBRARY: 702/3
CLONE: 12
FEATURE:
NAME/KEY: CDS
LOCATION: 85..1317
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 124..1314
OTHER INFORMATION:
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 85..123
OTHER INFORMATION:
PCT-US91-03478-12

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alignment_scores:
Quality: 307.00 Length: 345
Ratio: 1.574 Gaps: 14
Percent Similarity: 56.522 Percent Identity: 26.377

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seq_documentation_block:
  Sequence 3, Application US/08381603
  Patent No. 5858355
  GENERAL INFORMATION:
    APPLICANT: Giorioso, Joseph C.
    APPLICANT: Evans, Christopher H.
    APPLICANT: Robbins, Paul D.
    TITLE OF INVENTION: Gene Transfer For Treating a
    TITLE OF INVENTION: Mammalian Host
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Eckert Seamans Cherin & Mellott
      STREET: 1700 Market Street Suite 3232
      CITY: Philadelphia
      STATE: PA
      COUNTRY: USA
      ZIP: 19103
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA: 508/381,603
    APPLICATION NUMBER: US/08/381,603
    FILING DATE:
    CLASSIFICATION: 514
    ATTORNEY/AGENT INFORMATION:
      NAME: Gould, Jr., Lewis F.
      REGISTRATION NUMBER: 25,057
      REFERENCE/DOCKET NUMBER: 109070-11
      TELECOMMUNICATION INFORMATION:
        TELEPHONE: (215) 575-6000
        TELEFAX: (215) 575-6015
        TELEEX: 866172
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1782 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      HYPOTHETICAL: NO
      ANTI-SENSE: NO
      IMMEDIATE SOURCE:
        LIBRARY: Mouse T-cell cDNA Library
        CLONE: Mouse Interleukin-1 Receptor
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        NAME/KEY: CDS
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        US-08-381-603-3
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Percent Similarity: 54.908 Percent Identity: 25.767

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seq.name: /cgn2.6/pdata/1/lna/6A.COMB.seq:US-08-924-376-3

seq_documentation_block:
; Sequence 3, Application US/08924376
; Patent No. 6159464
; GENERAL INFORMATION:
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Evans, Christopher H.
; APPLICANT: Robbins, Paul D.
; APPLICANT: Bandera, Geethani
; TITLE OF INVENTION: Gene Transfer For Treating a
; TITLE OF INVENTION: Connective Tissue of a Mammalian Host
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,376
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/027,750
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 109070-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6000
; TELEFAX: (215) 575-6015
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Mouse T-cell cDNA library
; CLONE: Mouse Interleukin-1 Receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..1776
; US-08-924-376-3

alignment_scores:

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834 GAAGTGAATGATGCA.....
299 sncluser.....lleserhisserrargthr 307
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863 ATATGTCATTTCTAGTCGAGACATCATATTCATTTGCGAACATCCTTCAC 912
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seq_name: /cgn2_6/ptodata/1/ina/6B.COMB.seq:US-08-685-212-3

seq_documentation_block:
Sequence 3, Application US/08685212
Patent No. 6228356
GENERAL INFORMATION:
APPLICANT: Glorioso, Joseph C.
APPLICANT: Evans, Christopher H.
APPLICANT: Robbins, Paul D.
APPLICANT: Bandaru, Geetha
TITLE OF INVENTION: Gene Transfer For Treating a
TITLE OF INVENTION: Connective Tissue of a Mammalian Host
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street Suite 3232
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,212
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/027,750
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEFAX: (215) 575-6015
TELEX: 866172
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1782 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
LIBRARY: Mouse T-cell cDNA library
CLONE: Mouse Interleukin-1 Receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 46..1776
US-08-685-212-3

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Quality: 257.00 Length: 326
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 Percent Similarity: 54.908 Percent Identity: 25.767

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   88 oGluAsnArgIleSerLysGluLysAspValLeuThrPheArgProThrL 105
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   137 CysPheAsnSerProMetLysLeuProValHisLysLeuTyrrIleGluT 153
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   201 leAlaLeuIleSer.....AsnAsnGlyAsnTyrrCysValValThr 215
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   216 TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrVal 232
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834 GAAGTGAATGATCA.....GAAATGAATGA 862
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; Sequence 3, Application PC/TUS9402414
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh of the Commonwealth System of Higher Education
; TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02414
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 109070-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6000
; TELEFAX: (215) 575-6015
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Mouse T-cell cDNA library
; CLONE: Mouse Interleukin-1 Receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..1776
; PCT-US94-02414-3

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 Percent Similarity: 54.908 Percent Identity: 25.767

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55 yspheasnlyrSerThrAlaHisSerAlaGlyLeuThrleuIleTyr 71
206 AC.....GCCGACACCATAAATTTGCTAC 228
72 TrpThrlySglnAspArgAspLeuGluGluProIleAsnPheArgLeuP 88
229 .....AAGAATGACAGCAGACCCCATATACAGCGGAC...CG 263
88 ogluAsnArgIleSerlySglnuLysAspValleuTrpPheArgProThrL 105
264 GCACTCCAGATTCATCAGCAGATGCAATCTTGTGTTGTACTCGCA 313
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153 YrGlyIleGlnArgIleThrCysProAsnValAspGlyTyrPhe..... 167
460 .GGGAGTGAAGCTGTGTGCCCTATATGTG..AGTTATTTTAAAGAT 504
168 ProSerSerVallySProThrIleThrTrpTyrMetelYslySlyIle 184
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201 leAlaLeuIleSer.....AsnAsnGlyAsnlyrThrCysValValThr 215
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; Sequence 3, Application PC/TUS9608899
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh of the Commonwealth
; TITLE OF INVENTION: System of Higher Education
; TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue of a
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08899
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 109070-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6000
; TELEFAX: (215) 575-6015
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; LIBRARY: Mouse T-cell cDNA library
; CLONE: Mouse Interleukin-1 Receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 46..1776
; PCT-US96-08899-3

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alignment_scores:

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Quality: 257.00 Length: 326
Ratio: 1.436 Gaps: 17
Percent Similarity: 54.908 Percent Identity: 25.767

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alignment_block:
US-08-917-710-2 x PCR-US96-08899-3 ..

Align seg 1/1 to: PCT-US96-08899-3 from: 1 to: 1782

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; Sequence 3, Application US/07821716
; Patent No. 5319071
; GENERAL INFORMATION:
; APPLICANT: Dower, Steven K.
; APPLICANT: March, Carl J.
; APPLICANT: Sims, John
; TITLE OF INVENTION: Soluble Interleukin-1 Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/821,716
; FILING DATE: 19920114
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 125627
; FILING DATE: 25-NOV-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160550
; FILING DATE: 25-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 258756
; FILING DATE: 13-OCT-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 691551
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2001-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0606
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2356 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: mouse
; IMMEDIATE SOURCE:
; LIBRARY: MUILIR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 225..1955
; FEATURE:

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NAME/KEY: mat.peptide
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 US-07-821-716-3

alignment_scores:
 Quality: 257.00 Length: 326
 Ratio: 1.436 Gaps: 17
 Percent similarity: 54.908 Percent identity: 25.767

alignment_block:

US-08-917-710-2 x US-07-821-716-3

Align seg 1/1 to: US-07-821-716-3 from: 1 to: 2356

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323 rGluAspLeuLysArgSerTyValCys 332
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1142 CCAGTTTATGCGTATCCGTTTATCTGT 1169
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seq_name: /cgn2.6/prodata/1/ina/5A_COMB.seq:US-08-091-519-1
seq_documentation_block:
: Sequence 1, Application US/08091519
: Patent No. 5350683
: GENERAL INFORMATION:
: APPLICANT: Sims, John E.
: APPLICANT: Cosman, David J.
: APPLICANT: Lupton, Stephen D.
: APPLICANT: Mosley, Bruce A.
: APPLICANT: Dower, Steven K.
: TITLE OF INVENTION: Type II Interleukin-1 Receptors
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/091,519
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/701,415
: FILING DATE:
: APPLICATION NUMBER: US 07/534,193
: FILING DATE: 06-JUN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/573,576
: FILING DATE: 24-AUG-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/627,071
: FILING DATE: 13-DEC-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Wight, Christopher L.
: REGISTRATION NUMBER: 31680
: REFERENCE/DOCKET NUMBER: 2003-C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-5570
: TELEFAX: 206-233-0644
: INFORMATION FOR SEQ ID NO: 1:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEetical: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Human B cell lymphoblastoid
CELL LINE: CB23
IMMEDIATE SOURCE:
LIBRARY: CB23 cDNA
CLONE: PHIL-1R175
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OTHER INFORMATION:
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NAME/KEY: mat_peptide
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US-08-091-519-1

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Ratio: 1.383 Gaps: 13
Percent Similarity: 54.142 Percent Identity: 23.373

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Align seg 1/1 to: US-08-091-519-1 from: 1 to: 1357

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70 Trptryrtrptryrlysglnaspargaspleu...glugluuproileas 84
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118 Asnthrthryrlyserlyvalalapheroleuvalvalglnly 134
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487 AATGCTCTTACTGTGACAAATGTCATTGAGCTCAGAGTTTTTGGAA 536
134 saspsercysphaesnsrproleuylleuvalhisleuylr 151
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537 TACAGATGCTTTC.....CTGCCG.....TTCG 559
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604 GTATCCCTGACCTGAGTGAATTCACCCGTGACAAACTGACGTGAAGAT 653
175 eThrTrpTyrMetGlyCysTyrrlysilegluasnsrphesnasvalilep 192
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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192 rogluylmetasnsrphleuile.....Alaleuileser 205
704 TAAGTGTAGGGGAGCACCTCATCTACTGTACAGATGTGGCCCTGGAA 753
206 AsnAsnGlyAsnTyrrThrcysValValThrTyrrProgluasnglyargth 222
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754 GATGCTGGCTATTACCGCTGTCTCTGACATTTGCCATGAAGCCGACA 803
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272 eLeuMetAspSerArgAsnGluValTrpTrpThrleaspglylyslysp 289
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945 CGGCACACCTTAACACCATGCTGTGTGAGCGGCAAT..... 984
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316 .....LeuSerlleyslyvalThrSerGluaspleuylsa 328
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OM of: US-08-917-710-2 to: EST.* out-format: pfs
 Date: Jun 11, 2002 11:09 PM
 About: Results were produced by the Gencore software, version 4.5,
 Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame+2pn.model -DEV-xlh
 -Q/cgnt2.1/USPTO.spool/US0891710/runat.11062002.151026.18676/app-query.fasta.1.417
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 -FEAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
 -DELEXT=7.000 -START=1 -MATRIX=blonsum62 -TRANS=human40.cdi
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Search information block:

Query: US-08-917-710-2
 Query length: 356
 Database: EST.*
 Database sequences: 13736207
 Database length: 1841457050
 Search time (sec): 1690.340000

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 ACCESSION BC016141.1 GI:16359373
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1549)

late

REFERENCE
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@gscc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letlicia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Ulisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Series: IRAC Plate: 15 Row: 1 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4504660
 This clone has the following problem: frame shifted.

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17 nSerAspAlaSerGluArgCysAspAspTrpPheLeuAspThrMetArg 34
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256 AAGTATGCTCTCAGAACGCTCGATGACTGGGACTAGACACCATGAGGC 305
34 InIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
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306 AATTCAGAGTTTGAAGATGAGCCAGCTCCGATCAATGCTCCACTCTTT 355
51 GluHisPheLeuLysPheAsnTrpSerThrAlaHisSerAlaGluLeu 67
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356 GAACACTTCTTGAAATTCACATACACACACCCCATTCAGCTGGCTTAC 405
67 rLeuIleTrpTrpTrpThrLysGlnAspArgAspLeuGluProIleA 84
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101 PheArgProThrLeuLeuAsnAspTrpGlyAsnTrpThrCysMetLeu 117
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117 gAsnThrThrTrpCysSerLysValAlaPheProLeuGluValAlaGln 134
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556 GAACACTACATATTTGACGAAAGTGATTTCCCTTGGAAGTTGTTCAAA 605
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151 IleGluTrpGlyIleGlnArgIleThrCysProAsnValAspLysTrp 167
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167 eProSerValLysProThrIleThrTrpTrpMetGlyCysTrpLys 184
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VERSION    BI862501.1 GI:16003248
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            NIH-MGC http://mgi.nci.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: DCTP/DRP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
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150 CCCATGAACCTCCCACTGCATTAACGTATATAGAAATATGGCACTTAGAG 199

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849 bp mRNA linear EST 16-FEB-2001

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ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 849)	
JOURNAL	Ll,W.B., Gruber,C., Jasssee,J. and Polayes,D.	
COMMENT	Full-length cDNA libraries and normalization	
	Unpublished (2001)	
	Contact: Genoscope	
	Genoscope - Centre National de Sequencage	
	Bp 191 91006 EVRY cedex - France	
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	
FEATURES	Location/Qualifiers	
SOURCE	1..849	

BASE COUNT	232 a	206 c	185 g	224 t	2 others
ORIGIN					

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Quality	: 1286.00	Length: 247
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Percent Similarity	: 97.571	Percent Identity: 95.951

alignment_block:

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110 ATGACACTTGTGGTGGTGAAGTCTCACTTTATGAAATCTGCA 155
17 nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArg 34
160 AAGTAAGCTCCTCGAAGACGCTGGAGATGACTGGGAGCTATACACCATGAGGC 209
34 InitiGlnValPheGluAspGluProAlaArgIleGlyCysProLeuPhe 50
210 AAATTCACAGTGTTTGAAGATGAGCCAGCTGCATCAATGCCCACCTCTT 259
51 GluHisPheLeuLysPheAsnYrSerThrAlaHisSerAlaGlyLeu 67
260 GAACACTCTGTGAATTCACATCACACGACACCCATTCAGCTGCCTTAC 309
67 rLeuIleLeuPyrTrpThrLysGlnAspArgAspLeuGluProIleA 84
310 TCTGATCTGGTATGTGACTAGACGACGACCGGACCTTGAGAGCCAACTA 359
84 snPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
360 ACTTCGCGCTCCCCGAGAACCCGCACTAAGTAGAGGAAGAATGTCCTGTGG 409
101 PheArgProThrLeuAsnAspThrGlyAsnYrThrCysMetLeu 117
410 TTCGGCCCACTCTCTCAATGATACCTGGCAACTATACCTGCAGTTAAG 459

10

TITLE The Washu-HIMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira M/Mouse EST Project

COMMENT

Contact: Maria M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:971419
Seq primer: custom primer used
High quality sequence stop: 345.

BASE COUNT	ORIGIN	FEATURES	SOURCE
199 a	185 c	167 g	195 t
		10 others	

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US-08-917-710-2 x AI303998 ..
Align seg 1/1 to: AI303998 from: 1 to: 756
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 53 CtgTatGtGCTGGGACTtGATtACATGCGACAAATCCAAgTtTtTAAG 102
 40 sPgluProAlaArgIleuYcysProLeuPheGluHisPheLeuYsPhe 56
 103 ATGAGCGGGCTCGAATCAAGTtCCCGCTTtTGAACTtCTCGTAAGTAC 152
 57 AsnYtSerThrAlaHisSerIaGlyLeuThrIleTtPtytTtPh 73
 153 AACTtAGAGACTtGCCATtTCTtGGCTtTACCTtCCGACTtGTACTtGAGC 202
 73 tlysglnAspArgAspLeuGluGluProIleAsnPheArgLeuProGlu 90
 203 CAGGCAAGACCGGGACtGGAGAGACCATTtACTtCCGCTtCCCAAGGA 252
 90 snArgIleSerIySgluYsAspValLeuTtPheArgProThrLeuLeu 106
 253 ATCCGATCATGTAAGAGAAAGATGtGCTtGTtCCGGCCACCTtCTCTC 302
 107 AsnAspThrGlyAsnYtThrCysMetLeuArgAsnThrTtPtytYcysSe 123
 303 AATGACAGCGGCAATtTACCTtGCTtGtTtGGAGAACACAACTtTACTCGAG 352
 123 tlyValAlaPheProLeuGluValIaGlnIlyAspSerCysPheAsn 140
 353 CACACTtGCATtTCCCTtGGAAGTtTTCAGAAAGACAGCTtTTCATt 402
 140 ePpMetLeuYleuProValHisIySLeuYtIleGluYtGlyIleGln 156
 403 CTGGCATtAGATtCCCACTtGACACAAAGATtTATtTGAACATtGCATtCAT 452
 157 ArgIleThrCysProAsnValAspGlyTtYtPheProSerSerValIySpr 173
 453 AAGATCAATGTCCAAATGtTAGAGGATtACTtGCTtTCCAGtGTCAAGCC 502
 173 tThrIleThrTtPtytMetGlyCysYtIySleGlnAsnPheAsnAsnY 190
 503 ATCACTCACTtAGTATtAANGtNTGtACTGATtAGTtGAGACTtTTCATtATG 552
 190 alileProGluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsn 206
 553 TACTACMCNGAGGCAACTtTAGCTtNTTCACTtCTtGGTTTCAATA 602
 207 AsnGlyAsnYtThrCysValIaValTtYtProGluAsnGlyArgThrPh 223
 603 TAGGCAATATACACATGtGTGCTACATtATCCtGAAAACGAGAGCTtCTT 652
 223 eHisLeuThrArgTtThrLeuThrValIySValVal 234
 653 TCACCTtCACCAANGACTtGTGACTtGAATtGTGGTG 686
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 seq_documentation_block:
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 CDS 60285252861 NCI_CGAP_L49 Mus musculus cDNA clone IMAGE:5135287 5',
 mRNA sequence.
 CCESSION B1331848
 ERSION B1331848.1 GI:15016505
 EWORDS
 house mouse.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
MUS MUSCULUS	Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
1 (bases 1 to 888)				
NIH-MGC	http://mgs.nci.nih.gov/			
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: c9abs-remail.nih.gov				
Tissue Procurement: Jeffrey E. Green, M.D.				
cDNA Library Preparation: Life Technologies, Inc.				
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
plate: LLAM1332	row: h	column: 08		
High quality sequence stop: 802.				
Location/Qualifiers				
1. 888				
/organism="Mus musculus"				
/strain="FVB/N"				
/db_xref="taxon:10090"				
/clone="IMAGE:5135287"				
/clone_lib="NCI_CGAP_L19"				
/lab_host="DH10B (11 phage-resistant)"				
/note="Organ: Liver; Vector: PCMV-SPORE6; Site_1: NotI;				
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dn.				
Average insert size 1.9 kb. Constructed by Life				
Technologies. Note: this is a NCI_CGAP Library."				

FEATURES	source
BASE COUNT	217 a 227 c 219 g 225 t
ORIGIN	

alignment_scores:	Quality:	986.00	Length:	245
Ratio:	4.422		Gaps:	3
Percent Similarity:	91.020		Percent Identity:	79.592

alignment_block:	US-08-917-710-2	x	BI31848	..
Align seg 1/1	to: BI31848	from: 1	to: 888	

1	MetHleuLeuTrrpCysValValSerLeuYrrpHeYrGlyIleLeuG1	17
111		111
120	ATGGAGCTTGTGTGATTGATGAGATCTGCTCTATGAGATCGCA	169
17	nSerAspAlaSerGluArgCysAspAspTrpGlyLeuAspTrpMetArg	34
111		111
170	GAGCATCGTTGGAGCGGTGTGATGACTGGGAGACTAGATACCATGCGAC	219
34	lnIleGlnValPheGluAspGluProAlaArgIleLeuGlySerProLeuPhe	50
111		111
220	AAATCCAAAGTTTGAAGATGACCGCGTCGATCAAGGCCCTCTTT	269
51	GlnHisPheLeuLysPheAsnYrrSerTrpAlaHisSerAlaGlyLeuT	67
111		111
270	GAAACACTCTCGAAGTACAACTACACACTGCCCATCTCTGGCGTTAC	319
67	rLeuIleTrpYrTrpThrLysGlnAspArgAspLeuGluGluProIleA	84
111		111
320	CCTGATGTGTACTGCGACGACGCAAGACGCGGCTCGAGGAGGCCCATTA	369
84	snPheArgLeuProGluAsnArgIleSerLysGlnLysAspValLeuTrp	100
111		111
370	ACTTCCCGCTCCAGAGAAATCGATCGTAGGAGAAATGTGCTCTGG	419
101	PheArgProThrLeuLeuAsnAspTrpGlyAsnTrpThrCysMetLeuAr	117
111		111
420	TTCGGGCCAACCTCCCTCATGACAGGGCAATATACACTGCATGTTGAG	469
117	gAsnThrThrTyrcysSerLysValAlaPheProLeuGluValGlnL	134

ORIGIN

alignment_scores:

Quality: 937.00 Length: 177
Ratio: 5.294 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.435

alignment_block:

US-08-917-710-2 x AV656295 ..

Align seg 1/1 to: AV656295 from: 1 to: 596

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180 GlyCysTyrLysIleGlnAspHisAsnValIleProGluGlyMetAs 196
10 GGCTGTATATAAATACAGAAATTTATATATGTAATACCGAAGATATGA 59
196 nleuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysV 213
60 CTGAGATTTCCTCATTCCTTAATTTCAAAATATGGAATTAACACATGTG 109
213 AlValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeu 229
110 TTGTATACATATCCAGAAATGACCTACCTTTCATCTCACAGGACTCTG 159
230 ThrValLysValValGlySerProLysAsnAlaValProValIleHis 246
160 ACTGTAAGGTAGTACGCTCCCAAAAATGACAGTGCCTCTGTATCCA 209
246 sSerProAsnAspHisValValTyrGluLysGluProGlyLugluLeuL 263
210 TTCACCTATATGATCATGTGTCTATGAGAAAGAACCCAGAGAGAGCTAC 259
263 euIleProCysThrValTyrPheSerPheLeuMetAsSerArgAsnGlu 279
260 TCATTCCTGTACGGTCTATTTTGTGATGATGATTCCTGCAATGAG 309
280 ValTyrPThrIleAspGlyLysLysProAspAspIleThrIleAspVa 296
310 GTTGGTGACCATGATGAGAAAAAACCTGATGACATCACTATTGATGT 359
296 lThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgT 313
360 CACCATTTACGAAAGTATTAAGTCTATGAGAACAGAAAGATGAACAAGAA 409
313 hIleGlnIleLeuSerIleLysLysValThrSerGluAspLeuLysArgSer 329
410 CTCAGATTTTGAGCATCAAGAAAGTACCTCTGAGATCTCAAGCGCAGC 459
330 TyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaLaly 346
460 TATGTCTGTCTAGTCTAGAGAGCCAAAGGGCAAAATTCCAAGACGCCAA 509
346 sValLysGlnLysGlyAsnArgCysGlyGln 356
510 GGTGAACAGAAAGCTAATAGATGCGCTCAG 540

seq_name: gb_est2:BE892231

seq_documentation_block:
LOCUS BE892231 910 bp mRNA linear EST 20-OCT-2000
DEFINITION 601435065P1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920152 5',
MRNA sequence.
ACCESSION BE892231
VERSION BE892231.1 GI:10352355
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 910)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

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JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed, by: The I.M.A.G.E. Consortium (ILLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLN at:
http://image.llnl.gov
Plate: LLM9751 row: a column: 17
High quality sequence stop: 710.

FEATURES

source

Location/Qualifiers

1..910
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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 236 a 241 c 210 g 223 t

ORIGIN

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Quality: 924.00 Length: 249
Ratio: 4.667 Gaps: 4
Percent Similarity: 79.518 Percent Identity: 76.305

alignment_block:

US-08-917-710-2 x BE892231 ..

Align seg 1/1 to: BE892231 from: 1 to: 910

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17 nSerAspAlaSerGluArgCysAspAspThrPglYLeuAspThrMetArg 34
233 AATGATGCTTCAGAACCGCTGCCATGCTGGGAGACAGACCATGAGAGC 282
34 lIleGlnValPheGluAspGluProAlaArgIleLysCysProLeuPhe 50
283 AAATCCAAAGTGTGAAAGATGAGCCAGCTCGCATCAAGTCCACTCTTT 332
51 GluHisPheLeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuTh 67
333 GAACACTTCTTGAATTAACATACACACAGCCCAATTCAGTGGCCTTAC 382
67 lleuIleTrrTyrTrrThrLysGlnAspArgAspLeuGluGluProIleA 84
383 TCGATCTGTGATTTGACTAGCAGACCGGACCTTGAGGAGCCAAATTA 432
84 snPheArgLeuProGluAsnArgIleSerLysGlnLysAspValLeuTrrP 100
433 ACTTCCGCGCTCCCGAGAACCCGATTAAGAGAGAAAGATGCTGTGG 482
101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuAr 117
483 TTCGGGCCACTCTCTCATATGACACTGCAACTATACCTGCATGTTAG 532
117 gAsnThrThrTyrCysSerLysValAlaPheProLeuGluValGlnL 134
533 GAACACTACATATTGCAGCAAGTT.GCATTTCCCTTGGAAATGTTTCAA 581
134 yAspSerCysPhe AsnSerProMetLysLeuProValHisLys.LeuT 150
582 AAGACAGCTGTTCAAAATTCCTCCCATGAAGCTCCAGTGAACCTGT 631

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150 yrlleqlutyr. Glylleqlaargllethrcysproasnvalasglytyl 166
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 632 ATATGAAATATGCGATCAGAGATCATCTGTCCTCAATGTTGATGATGA 681
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 682 TTTTCTTCAGGT. AATCCAGCTATCTGTTATGAGGCTTATTA 730
 183 ysllleqlasnphesnasnalileprogluglymetasnleuserphe 199
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 731 AATACGACATTC..... 744
 200 leullealelleusernasnnglyasnlythrlycysvalalthrtyl 216
 745ATATGTA 752
 216 rprogluasnglyargthrpheslethrargthrleuthrvalysv 233
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 753 TACCGAAGTTGACCTGATTCGATCCCTTAATGCACTTATGATTCAT 802
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 803 GTGTGTCCTATCCGAATGGACATTCCTCCAGACCGCAT 843
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seq_documentation_block:
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 DEFINITION AV659167 GLC Homo sapiens cDNA clone G1CFUB08 3', mRNA sequence.
 ACCESSION AV659167
 VERSION AV659167.1 GI:9880181
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
 1 (bases 1 to 789)
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
 Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X.,
 Hu, G., Gu, J., Chen, Z., and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
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 Location/Qualifiers
 1..789
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 /dev_stage="Adult"
 /lab_host="SOLR"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 268 a 140 c 162 g 210 t 9 others
 ORIGIN

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Percent Similarity: 97.191 Percent Identity: 97.191

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 US-08-917-710-2 x AV659167 ..

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 48 GCGCTGTATTAATACGAAATTTTAAATGTAATACCCAGAGTAA 97
 196 nleuserpheullealelleusernasnnglyasnlythrlycysv 213
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 98 CTGAGTTCTCCTCATTCCTTAATTCAAATATGAAATATACACATG 147
 213 alyalthrtyrprogluasnglyarg. Thrphesleuthrargthrle 229
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 148 TTGTTACATATCCGAAATGAGACTGACCTTTCATCACCAGGACTCT 197
 229 uthrvalysvalalgyserprolysnalalvalprovalilleh 246
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 198 GACTGTAAAGTAGTAGGCTCTCCAAAAATGCGAGTCCCTGTGATCC 247
 246 lsserproasnphsivalalthrlyrglysgluuproglygluglu 262
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 248 ATTCACCTAATGATCATGTGCTATATGAAAGACAGAGAGAGACTA 297
 263 leulleprocystrhrvaltyrpheserpheleumetaspserar 279
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 298 CTCATTCCTCCGTACGCTCATATTATGTTCTGATGATTCCTCAATGA 347
 279 uvaltrptthrleaspglylyslsypaspsdilethrleaspv 296
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 348 GGTGTGTGACCATGATGAGAAAAAACCTGATGACATCTCTTATG 397
 296 althrleasnlguserlleuserhiserargthrgluaspgluthr 312
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 398 TCACCATTAACGAAGTATAGTCTATAGACAGAAAGATGAACAGA 447
 313 thrghilleuserllelyslsvalthrsergluaspleuysaryse 329
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 448 ACTCAGATTNTGAGCATCAGAAAGTACTCTGAGGATCTCAAGCGAG 497
 329 tlyrvalcyshisalaargseralalysgluvalalalyslaalal 346
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 498 CTATGCTGTCTATGCTAGAGATGCCAANAGCGCAAGTCCCAACAGCA 547
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 DEFINITION mw96b02.r1 Soares mouse NMU Mus musculus cDNA clone IMAGE:678507 5',
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 accessory (MUSE), mRNA sequence.

ACCESSION AA237107
 VERSION AA237107.1 GI:1861163
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT

Contact: Maria M/Mouse EST Project
 Washu-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL: contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:418211

FEATURES

Seq primer: -28m13 rev2 ET from Amer sham
 High quality sequence stop: 438.

source

Location/Qualifiers
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 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGGCGGGAATCTTTTCTTTTCTTTT
 TGTACCAATCTGAAGTGGAGCGGCGGGAATCTTTTCTTTTCTTTT
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7n3 vector. Library
 constructed and normalized by Bento Soares and M. Fatima
 Bonaldo."

BASE COUNT 161 a 146 c 137 g 153 t 1 others
 ORIGIN

alignment_scores:

Quality: 870.50 Length: 194
 Ratio: 4.836 Gaps: 1
 Percent Similarity: 92.784 Percent Identity: 80.928

alignment_block:

US-08-917-710-2 x AA237107 ..

Align seg 1/1 to: AA237107 from: 1 to: 598

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13 TCGGGCCTTACCTGATCTGTGACGACCAAGACGGGACCTGGA 62
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80 uGluProIleAsnPhetrleuproGluAsnArglleSerLysGluLysA 97
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63 GGAGCCCATTAACCTCCGCTCCCAAGAAATGCATCAAGAGAGAAAG 112
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
97 spValleuTrpPhetrpProThrleuAsnAspThrgLysAnrYrtrHr 113
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
113 ATGTCGCTGTCGCGGCCACCTCTCTCAATACACGGGCAATTTACACC 162
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114 CysMeleuArgAsnthrThrTyYsSerLysValAlaPheProLeuG1 130
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
163 TGGATGTGGAGAACAACTTACTCCAGCAAAAGTGCATTCCTCCCTGGA 212
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
130 uValValGlnLysAspSerCysPheAsnSerProMetLysIleuProValH 147
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
213 AGTGTTCAGAAAGACAGCTGTTCAATTTCTGCATGAAATTCCTCCAGTGC 262
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
147 IsLysLeuTrpIleGluTrpGlyIleGlnArgIleThrCysProAsnVal 163
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
263 ACAAGATGTAATATTGAACATGCATCATTAAGATCATGTCACAAATGTA 312
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164 AspGlyTrpPheProSerSerValLysProThrIleThrTrpYrMetG1 180
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313 GACGGTACTTCTCTCCAGTGCACAAACATGCATCTTGGTATAAAGG 362
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180 yCysTrpLysIleGlnAsnPhetrleuproGluLysIleuProValH 197
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197 euSerPheleuileAlaLeuileSerAsnAsnGlyAsnYrtrHrCysVal 213
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LOCUS BB625831 652 bp mRNA linear EST 31-AUG-2001
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 ACCESSION BB625831
 VERSION BB625831.1 GI:15398624
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 652)
 ARAKAWA,T., CARINCI,P., FUKUDA,S., FURUNO,M., HANAOKI,T., HARA,A.,
 HIRAMOTO,K., HORI,F., ISHII,Y., ITO,M., KAWAI,J., KONNO,H., KODA,
 M., KOYA,S., MATSUYAMA,T., MIYAZAKI,A., NOMURA,K., OHNO,M.,
 OKAZAKI,Y., OKIDO,T., SAITO,R., SAKAI,C., SAKAI,K., SANO,H., SASAKI,
 D., SHIBATA,K., SHINGAWA,A., SHIRAKI,T., SOGABE,Y., SUZUKI,H.,
 TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKEDA,Y., TANAKA,T., TOYA,T.,
 MURAMATSU,M. and HAYASHIZAKI,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,
 Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
 Ishii,Y. and Hayashizaki,Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Func. Genomics 2 pre, L72-L86 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for

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LOCUS AA107505 643 bp mRNA linear EST 04-NOV-1996

DEFINITION mp05d08.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA clone IMAGE:56835 5' similar to gb:x85999 M.musculus mRNA for interleukin 1 receptor accessory (MOUSE);, mRNA sequence.

ACCESSION AA107505

VERSION AA107505.1 GI:1659404

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The WashU-HM Mouse EST Project
 Unpublished (1996)
 Contact: Maria M/Mouse EST Project
 WashU-HM Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through INL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:342983
 Seq primer: -28M13 rev1 from Amersham
 High quality sequence stop: 454.
 Location/Qualifiers

SOURCE

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Wed Jun 12 09:27:08 2002

us-08-917-710-2.rst

Page 14

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DEFINITION	Homo sapiens soluble interleukin-1 receptor accessory protein (IL1RAP) mRNA, complete cds.								
ACCESSION	AF167343								
VERSION	AF167343.1	GI:8050486							
KEYWORDS									
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS	Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S.								
TITLE	IL-1 signaling cascade in liver cells and the involvement of a soluble form of the IL-1 receptor accessory protein								
JOURNAL	J. Immunol. 164 (10), 5277-5286 (2000)								
MEDLINE	20261666								
PUBMED	10799889								
REFERENCE	2 (bases 1 to 1857)								
AUTHORS	Jensen, L.E.								
TITLE	Direct Submission								
JOURNAL	Submitted (08-JUL-1999) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3420 Hamilton Walk, Philadelphia, PA 19104, USA								
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ACCESSION AR166115
VERSION AR166115.1 GI:16241289
KEYWORDS
SOURCE

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ORGANISM

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REFERENCE
1 (bases 1 to 1740)
AUTHORS

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TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
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JOURNAL Patent: US 6280935-A 1 28-AUG-2001;
FEATURES

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Location/Qualifiers

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LOCUS AF029213 1740 bp mRNA linear PRI 30-SEP-1999

DEFINITION Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.

ACCESSION AF029213

VERSION AF029213.1 GI:2599126

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1740)

AUTHORS Huang,J., Gao,X., Li,S. and Cao,Z.

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TITLE
JOURNAL Recruitment of IRAK to the interleukin 1 receptor complex requires
MEDLINE interleukin 1 receptor accessory protein
PUBMED Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
9371760
REFERENCE 2 (bases 1 to 1740)
AUTHORS Huang,J., Gao,X., Li,S. and Cao,Z.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1997) Biology, Tularek, Inc., 2 Corporate Dr.,
South San Francisco, CA 94080, USA
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REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) National Institutes of Health, Mammalian

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REMARK

COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES

source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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AUTHORS Cao, Z.
TITLE Interleukin-1 receptor accessory proteins, nucleic acids and
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REFERENCE 1 (bases 1 to 3355)
AUTHORS Submitted (31-MAR-1995) G.W. Ju, Hoffmann-La Roche Inc., 340
Kingsland Ave., Nutley, NJ 07110, USA
JOURNAL 2 (bases 1 to 3355)
AUTHORS Greenfeder,S.A., Nunes,P., Kwee,L., Labow,M., Chizzonite,R.A. and
Ju,G.
TITLE Molecular cloning and characterization of a second subunit of the
Interleukin 1 receptor complex
JOURNAL J. Biol. Chem. 270 (23), 13757-13765 (1995)
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VERSION AF167336.1 GI:8050492

KEYWORDS

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SOURCE human.

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REFERENCE 1 (bases 1 to 890)

AUTHORS Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S.

TITLE IL-1 signaling cascade in liver cells and the involvement of a soluble form of the IL-1 receptor accessory protein

JOURNAL J. Immunol. 164 (10), 5277-5286 (2000)

MEDLINE 20261666

PUBMED 10799889

REFERENCE 2 (bases 1 to 890)

AUTHORS Jensen, L.E.

TITLE Direct Submission

JOURNAL Submitted (09-JUL-1999) Department of Pharmacology, University of Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104, USA

FEATURES

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seq_name: gb_htg:AC108747

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seq_documentation_block: 160441 bp DNA linear HTG 31-JAN-2002

LOCUS AC108747

DEFINITION Homo sapiens chromosome 3 clone RP11-268E23, WORKING DRAFT

SEQUENCE, 14 unordered pieces.

ACCESSION AC108747

VERSION AC108747.1 GI:18449881

KEYWORDS

HTG: HTGS_PHASE1, HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 160441)

AUTHORS Muzny, D.M., Adams, C., Adio-Ondola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayala, M., Banks, T., Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gottrell, D.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
Honsi, F., Howard, S., Huber, J., Huliy, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, U., Kovar, C.,
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
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Miner, G., Miner, Z., Mitchell, T., Monabhat, K., Morgan, M., Morris, S.,
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Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
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Welnstock, G. and Gibbs, R.

Unpublished
2 (bases 1 to 160441)
Worley, K.C.
Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project information

Center project name: HDMO

Center clone name: RP11-268E23

Summary Statistics

Sequencing vector: Plasmid; M77789

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 159407 bases at least Q40

Consensus quality: 160755 bases at least Q30

Estimated insert size: 159008; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 14 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 50778: contig of 50778 bp in length
* 50779 50878: gap of unknown length
* 50779 72649: contig of 21771 bp in length
* 72650 72749: gap of unknown length
* 72750 86636: contig of 13887 bp in length
* 86637 86736: gap of unknown length
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* 104475 104574: gap of unknown length
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* 114932 119623: gap of unknown length
* 119623 119623: contig of 4692 bp in length

119624 119723: gap of unknown length
* 119724 124994: contig of 5271 bp in length
* 124995 125094: gap of unknown length
* 125095 130002: contig of 4908 bp in length
* 130003 130102: gap of unknown length
* 130103 137139: contig of 7036 bp in length
* 137139 137238: gap of unknown length
* 137239 143181: contig of 5943 bp in length
* 143182 143281: gap of unknown length
* 143282 147916: gap of unknown length
* 147916 148015: gap of unknown length
* 148016 153671: contig of 5656 bp in length
* 153672 153771: gap of unknown length
* 153772 156869: contig of 3098 bp in length
* 156870 156970: gap of unknown length
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FEATURES

source

BASE COUNT

ORIGIN

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Percent Similarity:

Percent Identity:

alignment_block:

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Align seg 1/1 to reverse of: AC108747 from: 1 to: 160441

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8096

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8046

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7996

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7946

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7896

105

7847

7846

seq_name: gb_pr: AC008249

seq_documentation_block:

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

184203 bp DNA linear PRI 28-OCT-1999

AC008249

3q27 BAC RP11-211P13 (Roswell Park Cancer Institute

Human BAC Library) complete sequence.

AC008249

AC008249.14 GI:6137875

HTG.

SOURCE

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 184203)

Muzny, D.M., Adams, C., Bailey, M., Barabara, J., Blankenburg, K.,
Bodola, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Garcia, D.K., Gorrell, J.H.,
Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J.,
Hodgson, A., Hogue, M., Holloway, C., Hosak, H., Jackson, L.E.,
Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondrjewski, N., Kong, Y.,
Kovar, C., Leal, B., Li, Z., Lichte, O., Liu, J., Liu, M., Logan, O.,
Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mel, G.,
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Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S.,
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Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M.,
Sparks, A., Stamps, A., Sugcang, R., Tabor, P., Taylor, T., Vasquez, L.,
Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstein, G.,
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Yu, W., Zhou, X., Zou, S.L., Nelson, D. and Gibbs, R.

TITLE
JOURNAL

Unpublished

REFERENCE
AUTHORS

2 (bases 1 to 184203)

TITLE
JOURNAL

Unpublished

REFERENCE
AUTHORS

Submitted (30-JUL-1999)

TITLE
JOURNAL

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS

3 (bases 1 to 184203)

TITLE
JOURNAL

Submitted (28-OCT-1999)

REFERENCE
AUTHORS

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Oct 28, 1999 this sequence version replaced gi:6091634.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features Listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality_info/genbank_annotation.html.

QUALSTAT-REPORT-----

Summary Statistics									
Contig length:		184203							
Phrap values in estimate:		183529							
Average error rate (BCM-Phrap estimate):		1.29501e-05							
Fraction of Phrap values less than 40 :		0.0125648							
Number of consensus changing edits:		4							
Number of N's in consensus :		0							
----- Distribution of Quality < 40 Bases -----									
Position	Original+Context	Edited+Context							
6949	aaggagactg(n)acaactctt	aaggagactg(c)acaactctt							
148395	tctattatg(n)tttattctct	tctattatg(t)tttattctct							
171291	gagagaagaa(n)caactgacta	gagagaagaa(a)caactgacta							
171310	taaggcatga(n)agcaatagg	taaggcatga(a)agcaatagg							

#	bases	1000	900	800	700	600	500	400	300
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		5	10	15	20	25	30	35	40
		Phrap Value Range							

Version: 1.01 gqfo.									
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DEFINITION Homo sapiens mRNA for ILIRAPL-2 related protein.
ACCESSION  AJ290436
VERSION    AJ290436.1 GI:7688204
KEYWORDS   ILIRAPL-2 gene; ILIRAPL-2 related protein.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (sites)
            Ferrante,M.I., Ghiani,M., Bulfone,A. and Franco,B.
            ILIRAPL2 maps to Xq22 and is specifically expressed in the central
            nervous system
            Gene 275 (2), 217-221 (2001)
2 (bases 1 to 2080)
            Ferrante,M.
            Direct Submission
            Submitted (02-MAY-2000) Ferrante M., Telethon Institute of
            Genetics and Medicine, via Olgettina, 58, 20132 Milano, ITALY
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83 leaSnPheArgLeuProGlnAsnArgLleSerLysGlnLysAspValLeu 99
279 TCATCTTT.....TCAGAGGTCACAGATGACCAAGAGGAATTCATA 322
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323 TGGTTTCACCTACAGCTAGGACACAGACAGTGGATTCTACACTGGTGTTT 372
116 uArgAsnThrThrTyTrpCysSerLysValAlaPheProLeuGlnValValG 133
373 AAGAACTCAACATATTTGGATGAAGGTGTGCATGTCTTCATGCTGGTCAG 422
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423 AGAATGATCAGGCGCTGTGCTACCAACAGCAGGATCCG..... 466
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461 .....TATTGAAAGAAATCTGAAGTCACTAAAGAAAGACATCTCTG 504
160 sProAsnValAspGlyTyTrpPheProSerSerValLysProThrIleThrT 177
505 TCCAGACATGAGATGACTTAAAGATGCGATCAGGAGCCGTGTTGGT 554
177 rPyrMetGlyCysTyTrpLleGlnAsnPheAsnValLleProLu 199
555 GGTATGAGATGCGAGGCCAAATAATGGAGAGCATTAATTAATACAGAA 604
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[illegible]

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DEFINITION Homo sapiens TIGIR-1 mRNA, complete cds.
ACCESSION AF284436
VERSION AF284436.1 GI:10644689
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2212)
AUTHORS Born,T.L., Smith,D.E., Garke,K.E., Renshaw,B.R., Bertles,J.S. and
Sims,J.E.
TITLE Identification and characterization of two members of a novel class
of the interleukin-1 receptor (IL-1R) family. Delineation of a new
class of IL-1R-related proteins based on signaling
JOURNAL J. Biol. Chem. 275 (39), 29946-29954 (2000)
MEDLINE 20459050
REFERENCE 2 (bases 1 to 2212)
AUTHORS Born,T.L., Smith,D.E., Garke,K.E., Renshaw,B.R., Bertles,J.S. and
Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2000) Molecular Biology, Immunex Corp, 51
University St., Seattle, WA 98101-2936, USA
FEATURES
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ORIGIN

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US-08-917-710-2 x AF284436 ..
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33 rGlnIleGlnValPheGluAspGluProAlaArgIleCysProLeu 49
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DEFINITION Homo sapiens mRNA for IL-1 receptor accessory protein-like 2
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ACCESSION AJ272208
VERSION AJ272208.1 GI:7530096
KEYWORDS IL1RAPL-2 gene.
SOURCE human.
ORGANISM Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2985)
AUTHORS Grabowski,M., Lorenz,B., Hubel,R. and Strom,T.M.
TITLE A gene (IL1RAPL-2) with 61% identity to IL1RAPL maps to Xq22.2
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 2985)
STREAM T.M.
TITLE Direct Submission
AUTHORS Submitted (14-FEB-2000) Strom T.M., Medizinische Genetik,
JOURNAL Goethestr. 29, Muenchen 80336, GERMANY
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